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RAW SEQUENCE LISTING

DATE: 02/27/2003

PATENT APPLICATION: US/09/857,123A

TIME: 10:56:32

Input Set : A:\Pg3606SEQLIST.txt

Output Set: N:\CRF4\02272003\I857123A.raw

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4 <110> APPLICANT: Glaxo Group Ltd
5     Tate, Simon N
6     Delany, Natalie S
7     Sanseau, P
9 <120> TITLE OF INVENTION: Novel Receptors
11 <130> FILE REFERENCE: PG3606
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/857,123A
C--> 14 <141> CURRENT FILING DATE: 2000-06-01
16 <150> PRIOR APPLICATION NUMBER: GB 9826359.3
17 <151> PRIOR FILING DATE: 1998-12-01
19 <160> NUMBER OF SEQ ID NOS: 40
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4365
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
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44 ccatacctcat caccgagatc ctccctgaat tcagcccacg acagccaccc cggccgtttt 360
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56 ccttggaag gagggcagg ggggtctaag gacaagcagt ccttactttg ggagtcaacc 720
58 ccggcgtggt ggctgctgca ggttgcacac tgggccacag aggatccagc aagg atg 777
59                                     Met
60                                     1
62 aag aaa tgg agc agc aca gac ttg ggg gca gct gcg gac cca ctc caa 825
63 Lys Lys Trp Ser Ser Thr Asp Leu Gly Ala Ala Ala Asp Pro Leu Gln
64     5                                10                                15
66 aag gac acc tgc cca gac ccc ctg gat gga gac cct aac tcc agg cca 873
67 Lys Asp Thr Cys Pro Asp Pro Leu Asp Gly Asp Pro Asn Ser Arg Pro
68     20                                25                                30
70 cct cca gcc aag ccc cag ctc tcc acg gcc aag agc cgc acc cgg ctc 921
71 Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg Leu

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75	Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro His			
76	50 55 60 65			
79	gag gaa ggt gag ctg gac tcc tgc ccg acc atc aca gtc agc cct gtt	1017		
80	Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro Val			
81	70 75 80			
83	atc acc atc cag agg cca gga gac ggc ccc acc ggt gcc agg ctg ctg	1065		
84	Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu Leu			
85	85 90 95			
87	tcc cag gac tct gtc gcc gcc agc acc gag aag acc ctc agg ctc tat	1113		
88	Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu Tyr			
89	100 105 110			
91	gat cgc agg agt atc ttt gaa gcc gtt gct cag aat aac tgc cag gat	1161		
92	Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln Asp			
93	115 120 125			
95	ctg gag agc ctg ctg ctc ttc ctg cag aag agc aag aag cac ctc aca	1209		
96	Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu Thr			
97	130 135 140 145			
99	gac aac gag ttc aaa gac cct gag aca ggg aag acc tgt ctg ctg aaa	1257		
100	Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu Lys			
101	150 155 160			
103	gcc atg ctc aac ctg cac gac gga cag aac acc acc atc ccc ctg ctc	1305		
104	Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu Leu			
105	165 170 175			
107	ctg gag atc gcg cgg caa acg gac agc ctg aag gag ctt gtc aac gcc	1353		
108	Leu Glu Ile Ala Arg Gln Thr Asp Ser Leu Lys Glu Leu Val Asn Ala			
109	180 185 190			
111	agc tac acg gac agc tac tac aag ggc cag aca gca ctg cac atc gcc	1401		
112	Ser Tyr Thr Asp Ser Tyr Tyr Lys Gly Gln Thr Ala Leu His Ile Ala			
113	195 200 205			
116	atc gag aga cgc aac atg gcc ctg gtg acc ctc ctg gtg gag aac gga	1449		
117	Ile Glu Arg Arg Asn Met Ala Leu Val Thr Leu Leu Val Glu Asn Gly			
118	210 215 220 225			
120	gca gac gtc cag gct gcg gcc cat ggg gac ttc ttt aag aaa acc aaa	1497		
121	Ala Asp Val Gln Ala Ala Ala His Gly Asp Phe Phe Lys Lys Thr Lys			
122	230 235 240			
124	ggg cgg cct gga ttc tac ttc ggt gaa ctg ccc ctg tcc ctg gcc gcg	1545		
125	Gly Arg Pro Gly Phe Tyr Phe Gly Glu Leu Pro Leu Ser Leu Ala Ala			
126	245 250 255			
128	tgc acc aac cag ctg ggc atc gtg aag ttc ctg ctg cag aac tcc tgg	1593		
129	Cys Thr Asn Gln Leu Gly Ile Val Lys Phe Leu Leu Gln Asn Ser Trp			
130	260 265 270			
132	cag acg gcc gac atc agc gcc agg gac tcg gtg ggc aac acg gtg ctg	1641		
133	Gln Thr Ala Asp Ile Ser Ala Arg Asp Ser Val Gly Asn Thr Val Leu			
134	275 280 285			
136	cac gcc ctg gtg gag gtg gcc gac aac acg gcc gac aac acg aag ttt	1689		
137	His Ala Leu Val Glu Val Ala Asp Asn Thr Ala Asp Asn Thr Lys Phe			
138	290 295 300 305			

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141	Val	Thr	Ser	Met	Tyr	Asn	Glu	Ile	Leu	Ile	Leu	Gly	Ala	Lys	Leu	His	
142					310					315					320		
144	ccg	acg	ctg	aag	ctg	gag	gag	ctc	acc	aac	aag	aag	gga	atg	acg	ccg	1785
145	Pro	Thr	Leu	Lys	Leu	Glu	Glu	Leu	Thr	Asn	Lys	Lys	Gly	Met	Thr	Pro	
146				325						330					335		
148	ctg	gct	ctg	gca	gct	ggg	acc	ggg	aag	atc	ggg	gtc	ttg	gcc	tat	att	1833
149	Leu	Ala	Leu	Ala	Ala	Gly	Thr	Gly	Lys	Ile	Gly	Val	Leu	Ala	Tyr	Ile	
150			340					345					350				
153	ctc	cag	cgg	gag	atc	cag	gag	ccc	gag	tgc	agg	cac	ctg	tcc	agg	aag	1881
154	Leu	Gln	Arg	Glu	Ile	Gln	Glu	Pro	Glu	Cys	Arg	His	Leu	Ser	Arg	Lys	
155		355					360					365					
157	ttc	acc	gag	tgg	gcc	tac	ggg	ccc	gtg	cac	tcc	tcg	ctg	tac	gac	ctg	1929
158	Phe	Thr	Glu	Trp	Ala	Tyr	Gly	Pro	Val	His	Ser	Ser	Leu	Tyr	Asp	Leu	
159	370					375					380				385		
161	tcc	tgc	atc	gac	acc	tgc	gag	aag	aac	tcg	gtg	ctg	gag	gtg	atc	gcc	1977
162	Ser	Cys	Ile	Asp	Thr	Cys	Glu	Lys	Asn	Ser	Val	Leu	Glu	Val	Ile	Ala	
163				390						395					400		
165	tac	agc	agc	agc	gag	acc	cct	aat	cgc	cac	gac	atg	ctc	ttg	gtg	gag	2025
166	Tyr	Ser	Ser	Ser	Glu	Thr	Pro	Asn	Arg	His	Asp	Met	Leu	Leu	Val	Glu	
167			405					410					415				
169	ccg	ctg	aac	cga	ctc	ctg	cag	gac	aag	tgg	gac	aga	ttc	gtc	aag	cgc	2073
170	Pro	Leu	Asn	Arg	Leu	Leu	Gln	Asp	Lys	Trp	Asp	Arg	Phe	Val	Lys	Arg	
171		420						425					430				
173	atc	ttc	tac	ttc	aac	ttc	ctg	gtc	tac	tgc	ctg	tac	atg	atc	atc	ttc	2121
174	Ile	Phe	Tyr	Phe	Asn	Phe	Leu	Val	Tyr	Cys	Leu	Tyr	Met	Ile	Ile	Phe	
175		435				440						445					
177	acc	atg	gct	gcc	tac	tac	agg	ccc	gtg	gat	ggc	ttg	cct	ccc	ttt	aag	2169
178	Thr	Met	Ala	Ala	Tyr	Tyr	Arg	Pro	Val	Asp	Gly	Leu	Pro	Pro	Phe	Lys	
179	450					455					460				465		
181	atg	gaa	aaa	att	gga	gac	tat	ttc	cga	gtt	act	gga	gag	atc	ctg	tct	2217
182	Met	Glu	Lys	Ile	Gly	Asp	Tyr	Phe	Arg	Val	Thr	Gly	Glu	Ile	Leu	Ser	
183				470						475					480		
185	gtg	tta	gga	gga	gtc	tac	ttc	ttt	ttc	cga	ggg	att	cag	tat	ttc	ctg	2265
186	Val	Leu	Gly	Gly	Val	Tyr	Phe	Phe	Phe	Arg	Gly	Ile	Gln	Tyr	Phe	Leu	
187			485					490					495				
190	cag	agg	cgg	ccg	tcg	atg	aag	acc	ctg	ttt	gtg	gac	agc	tac	agt	gag	2313
191	Gln	Arg	Arg	Pro	Ser	Met	Lys	Thr	Leu	Phe	Val	Asp	Ser	Tyr	Ser	Glu	
192			500					505					510				
194	atg	ctt	ttc	ttt	ctg	cag	tca	ctg	ttc	atg	ctg	gcc	acc	gtg	gtg	ctg	2361
195	Met	Leu	Phe	Phe	Leu	Gln	Ser	Leu	Phe	Met	Leu	Ala	Thr	Val	Val	Leu	
196		515					520					525					
198	tac	ttc	agc	cac	ctc	aag	gag	tat	gtg	gct	tcc	atg	gta	ttc	tcc	ctg	2409
199	Tyr	Phe	Ser	His	Leu	Lys	Glu	Tyr	Val	Ala	Ser	Met	Val	Phe	Ser	Leu	
200	530					535					540				545		
202	gcc	ttg	ggc	tgg	acc	aac	atg	ctc	tac	tac	acc	cgc	ggg	ttc	cag	cag	2457
203	Ala	Leu	Gly	Trp	Thr	Asn	Met	Leu	Tyr	Tyr	Thr	Arg	Gly	Phe	Gln	Gln	
204				550						555					560		
206	atg	ggc	atc	tat	gcc	gtc	atg	ata	gag	aag	atg	atc	ctg	aga	gac	ctg	2505

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210	tgc	cgt	ttc	atg	ttt	gtc	tac	atc	gtc	ttc	ttg	ttc	ggg	ttt	tcc	aca	2553
211	Cys	Arg	Phe	Met	Phe	Val	Tyr	Ile	Val	Phe	Leu	Phe	Gly	Phe	Ser	Thr	
212			580						585					590			
214	gcg	gtg	gtg	acg	ctg	att	gaa	gac	ggg	aag	aat	gac	tcc	ctg	ccg	tct	2601
215	Ala	Val	Val	Thr	Leu	Ile	Glu	Asp	Gly	Lys	Asn	Asp	Ser	Leu	Pro	Ser	
216			595					600					605				
218	gag	tcc	acg	tcg	cac	agg	tgg	cgg	ggg	cct	gcc	tgc	agg	ccc	ccc	gat	2649
219	Glu	Ser	Thr	Ser	His	Arg	Trp	Arg	Gly	Pro	Ala	Cys	Arg	Pro	Pro	Asp	
220	610					615					620					625	
222	agc	tcc	tac	aac	agc	ctg	tac	tcc	acc	tgc	ctg	gag	ctg	ttc	aag	ttc	2697
223	Ser	Ser	Tyr	Asn	Ser	Leu	Tyr	Ser	Thr	Cys	Leu	Glu	Leu	Phe	Lys	Phe	
224				630						635					640		
227	acc	atc	ggc	atg	ggc	gac	ctg	gag	ttc	act	gag	aac	tat	gac	ttc	aag	2745
228	Thr	Ile	Gly	Met	Gly	Asp	Leu	Glu	Phe	Thr	Glu	Asn	Tyr	Asp	Phe	Lys	
229				645						650					655		
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233			660						665					670			
235	ctc	ctg	ctc	aac	atg	ctc	atc	gcc	ctc	atg	ggt	gag	act	gtc	aac	aag	2841
236	Leu	Leu	Leu	Asn	Met	Leu	Ile	Ala	Leu	Met	Gly	Glu	Thr	Val	Asn	Lys	
237			675					680					685				
239	atc	gca	cag	gag	agc	aag	aac	atc	tgg	aag	ctg	cag	aga	gcc	atc	acc	2889
240	Ile	Ala	Gln	Glu	Ser	Lys	Asn	Ile	Trp	Lys	Leu	Gln	Arg	Ala	Ile	Thr	
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243	atc	ctg	gac	acg	gag	aag	agc	ttc	ctt	aag	tgc	atg	agg	aag	gcc	ttc	2937
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247	cgc	tca	ggc	aag	ctg	ctg	cag	gtg	ggg	tac	aca	cct	gat	ggc	aag	gac	2985
248	Arg	Ser	Gly	Lys	Leu	Leu	Gln	Val	Gly	Tyr	Thr	Pro	Asp	Gly	Lys	Asp	
249				725						730					735		
251	gac	tac	cgg	tgg	tgc	ttc	agg	gtg	gac	gag	gtg	aac	tgg	acc	acc	tgg	3033
252	Asp	Tyr	Arg	Trp	Cys	Phe	Arg	Val	Asp	Glu	Val	Asn	Trp	Thr	Thr	Trp	
253			740						745					750			
255	aac	acc	aac	gtg	ggc	atc	atc	aac	gaa	gac	ccg	ggc	aac	tgt	gag	ggc	3081
256	Asn	Thr	Asn	Val	Gly	Ile	Ile	Asn	Glu	Asp	Pro	Gly	Asn	Cys	Glu	Gly	
257			755					760					765				
259	gtc	aag	cgc	acc	ctg	agc	ttc	tcc	ctg	cgg	tca	agc	aga	gtt	tca	ggc	3129
260	Val	Lys	Arg	Thr	Leu	Ser	Phe	Ser	Leu	Arg	Ser	Ser	Arg	Val	Ser	Gly	
261	770					775					780					785	
264	aga	cac	tgg	aag	aac	ttt	gcc	ctg	gtc	ccc	ctt	tta	aga	gag	gca	agt	3177
265	Arg	His	Trp	Lys	Asn	Phe	Ala	Leu	Val	Pro	Leu	Leu	Arg	Glu	Ala	Ser	
266				790						795					800		
268	gct	cga	gat	agg	cag	tct	gct	cag	ccc	gag	gaa	gtt	tat	ctg	cga	cag	3225
269	Ala	Arg	Asp	Arg	Gln	Ser	Ala	Gln	Pro	Glu	Glu	Val	Tyr	Leu	Arg	Gln	
270				805						810					815		
272	ttt	tca	ggg	tct	ctg	aag	cca	gag	gac	gct	gag	gtc	ttc	aag	agt	cct	3273
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276 gcc gct tcc ggg gag aag tga ggacgtcacg cagacagcac tgtcaacact      3324
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280 gggccttagg agaccccgtt gccacggggg gctgctgagg gaacaccagt gctctgtcag 3384
282 cagcctggcc tggctctgtgc ctgcccagca tgttcccaa tctgtgctgg acaagctgtg 3444
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286 atctcctaag agactttcag gtttttactc actttactaa acagtttgga tggtcagtct 3564
288 ctactgggac atgttaggcc cttgttttct ttgattttat tcttttctgt gagacagagt 3624
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330 Pro Pro Pro Ala Lys Pro Gln Leu Ser Thr Ala Lys Ser Arg Thr Arg
331 35 40 45
333 Leu Phe Gly Lys Gly Asp Ser Glu Glu Ala Phe Pro Val Asp Cys Pro
334 50 55 60
336 His Glu Glu Gly Glu Leu Asp Ser Cys Pro Thr Ile Thr Val Ser Pro
337 65 70 75 80
339 Val Ile Thr Ile Gln Arg Pro Gly Asp Gly Pro Thr Gly Ala Arg Leu
340 85 90 95
342 Leu Ser Gln Asp Ser Val Ala Ala Ser Thr Glu Lys Thr Leu Arg Leu
343 100 105 110
345 Tyr Asp Arg Arg Ser Ile Phe Glu Ala Val Ala Gln Asn Asn Cys Gln
346 115 120 125
348 Asp Leu Glu Ser Leu Leu Leu Phe Leu Gln Lys Ser Lys Lys His Leu
349 130 135 140
351 Thr Asp Asn Glu Phe Lys Asp Pro Glu Thr Gly Lys Thr Cys Leu Leu
352 145 150 155 160
354 Lys Ala Met Leu Asn Leu His Asp Gly Gln Asn Thr Thr Ile Pro Leu
355 165 170 175

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L:13 M:270 C: Current Application Number differs, Replaced Application Number

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date